



1600

Does Not Comply
Corrected Diskette Needed

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/469,200C

DATE: 09/05/2002
TIME: 08:43:23

Errors on p. 3

Input Set : A:\sequence listing.txt
Output Set: N:\CRF4\09052002\I469200C.raw

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3 <110> APPLICANT: Weigel, Paul H.
4   DeAngelis, Paul
5   Kumari, Kshama
7 <120> TITLE OF INVENTION: Hyaluronan Synthase Gene and Uses Thereof
9 <130> FILE REFERENCE: 3554.011
11 <140> CURRENT APPLICATION NUMBER: US 09/469,200C
12 <141> CURRENT FILING DATE: 1999-12-21
14 <150> PRIOR APPLICATION NUMBER: US 09/178,851
15 <151> PRIOR FILING DATE: 1998-10-26
17 <150> PRIOR APPLICATION NUMBER: US 60/064,435
18 <151> PRIOR FILING DATE: 1997-10-31
20 <160> NUMBER OF SEQ ID NOS: 10
22 <170> SOFTWARE: PatentIn version 3.1
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 1254
26 <212> TYPE: DNA
27 <213> ORGANISM: Streptococcus equisimilis
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32 atttacgtca atgtttatct ctttgggtgt aaaggaagct tgtcaattta tggctttttg      120
34 ctgatagctt acctattagt caaaatgtcc ttatcctttt tttacaagcc atttaaggga      180
36 agggctgggc aatataaggt tgcagccatt attcctctct ataacgaaga tgctgagtca      240
38 ttgctagaga ccttaaaaaag tggtcagcag caaacctatc ccctagcaga aatttatggt      300
40 gttgacgatg gaagtgctga tgagacaggt attaagcgca ttgaagacta tgtgcgtgac      360
42 actggtgacc tatcaagcaa tgtcattggt catcggtcag agaaaaatca aggaaagcgt      420
44 catgcacagg cctgggcctt tgaaagatca gacgctgatg tctttttgac cgttgactca      480
46 gatacttata tctacctga tgcttttagag gagttgttaa aaacctttta tgaccaact      540
48 gtttttgctg cgacgggtca ccttaatgtc agaaatagac aaaccaatct cttaacacgc      600
50 ttgacagata ttcgctatga taatgctttt ggcgttgaa gagctgcca atccgttaca      660
52 ggtaatatcc ttgtttgctc aggtccgctt agcgtttaca gacgcgaggt ggttgttcct      720
54 aacatagata gatacatcaa ccagaccctc ctgggtattc ctgtaagtat tggatgac      780
56 aggtgcttga ccaactatgc aactgattta ggaaagactg tttatcaatc cactgctaaa      840
58 tgtattacag atgttcctga caagatgtct acttacttga agcagcaaaa ccgctggaac      900
60 aagtccttct ttagagagtc cattatttct gttaagaaaa tcatgaacaa tccttttgta      960
62 gccctatgga ccatacttga ggtgtctatg tttatgatgc ttgtttatc tgtggtgat      1020
64 ttctttgtag gcaatgtcag agaatttgat tggctcaggg ttttagcctt tctggtgatt      1080
66 atcttcattg ttgccctgtg tcggaacatt cattacatgc ttaagcacc gctgtccttc      1140
68 ttgttatctc cgttttatgg ggtgctgcat ttgtttgtcc tacagccctt gaaattatat      1200
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74 <211> LENGTH: 417
75 <212> TYPE: PRT
76 <213> ORGANISM: Streptococcus Equisimilis

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81 1      5      10      15
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85      20      25      30
88 Ser Leu Ser Ile Tyr Gly Phe Leu Leu Ile Ala Tyr Leu Leu Val Lys
89      35      40      45
92 Met Ser Leu Ser Phe Phe Tyr Lys Pro Phe Lys Gly Arg Ala Gly Gln
93      50      55      60
96 Tyr Lys Val Ala Ala Ile Ile Pro Ser Tyr Asn Glu Asp Ala Glu Ser
97 65      70      75      80
100 Leu Leu Glu Thr Leu Lys Ser Val Gln Gln Gln Thr Tyr Pro Leu Ala
101      85      90      95
104 Glu Ile Tyr Val Val Asp Asp Gly Ser Ala Asp Glu Thr Gly Ile Lys
105      100      105      110
108 Arg Ile Glu Asp Tyr Val Arg Asp Thr Gly Asp Leu Ser Ser Asn Val
109      115      120      125
112 Ile Val His Arg Ser Glu Lys Asn Gln Gly Lys Arg His Ala Gln Ala
113      130      135      140
116 Trp Ala Phe Glu Arg Ser Asp Ala Asp Val Phe Leu Thr Val Asp Ser
117 145      150      155      160
120 Asp Thr Tyr Ile Tyr Pro Asp Ala Leu Glu Glu Leu Leu Lys Thr Phe
121      165      170      175
124 Asn Asp Pro Thr Val Phe Ala Ala Thr Gly His Leu Asn Val Arg Asn
125      180      185      190
128 Arg Gln Thr Asn Leu Leu Thr Arg Leu Thr Asp Ile Arg Tyr Asp Asn
129      195      200      205
132 Ala Phe Gly Val Glu Arg Ala Ala Gln Ser Val Thr Gly Asn Ile Leu
133      210      215      220
136 Val Cys Ser Gly Pro Leu Ser Val Tyr Arg Arg Glu Val Val Val Pro
137 225      230      235      240
140 Asn Ile Asp Arg Tyr Ile Asn Gln Thr Phe Leu Gly Ile Pro Val Ser
141      245      250      255
144 Ile Gly Asp Asp Arg Cys Leu Thr Asn Tyr Ala Thr Asp Leu Gly Lys
145      260      265      270
148 Thr Val Tyr Gln Ser Thr Ala Lys Cys Ile Thr Asp Val Pro Asp Lys
149      275      280      285
152 Met Ser Thr Tyr Leu Lys Gln Gln Asn Arg Trp Asn Lys Ser Phe Phe
153      290      295      300
156 Arg Glu Ser Ile Ile Ser Val Lys Lys Ile Met Asn Asn Pro Phe Val
157 305      310      315      320
160 Ala Leu Trp Thr Ile Leu Glu Val Ser Met Phe Met Met Leu Val Tyr
161      325      330      335
164 Ser Val Val Asp Phe Phe Val Gly Asn Val Arg Glu Phe Asp Trp Leu
165      340      345      350
168 Arg Val Leu Ala Phe Leu Val Ile Ile Phe Ile Val Ala Leu Cys Arg
169      355      360      365
172 Asn Ile His Tyr Met Leu Lys His Pro Leu Ser Phe Leu Leu Ser Pro
173      370      375      380

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176 Phe Tyr Gly Val Leu His Leu Phe Val Leu Gln Pro Leu Lys Leu Tyr
 177 385 390 395 400
 180 Ser Leu Phe Thr Ile Arg Asn Ala Asp Trp Gly Thr Arg Lys Lys Leu
 181 405 410 415
 184 Leu
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 189 <211> LENGTH: 22
 190 <212> TYPE: DNA
 191 <213> ORGANISM: Synthetic
 193 <400> SEQUENCE: 3
 194 gctgatgaga caggtattaa gc
 197 <210> SEQ ID NO: 4
 198 <211> LENGTH: 20
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 200 <213> ORGANISM: Synthetic
 202 <400> SEQUENCE: 4
 203 atcaaattct ctgacattgc
 206 <210> SEQ ID NO: 5
 207 <211> LENGTH: 20
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 209 <213> ORGANISM: Synthetic
 211 <400> SEQUENCE: 5
 212 gactcagata cttatatcta
 215 <210> SEQ ID NO: 6
 216 <211> LENGTH: 17
 217 <212> TYPE: DNA
 218 <213> ORGANISM: Synthetic
 220 <400> SEQUENCE: 6
 221 tttttacgtg ttcccca
 224 <210> SEQ ID NO: 7
 225 <211> LENGTH: 1740
 226 <212> TYPE: DNA
 227 <213> ORGANISM: Paramecium bursaria chlorella virus
 229 <400> SEQUENCE: 7
 230 aagacttctt gaaagttaca atgggtaaaa atataatcat aatggtttcg tggtaacca 60
 232 tcataacttc aaatctaata gcggttggag gagcctctct aatcttggct ccggcaatta 120
 234 ctgggtatgt tctacattgg aatattgctc tctcgacaat ctggggagta tcagcttatg 180
 236 gtattttcgt ttttgggttt ttccttgacac aagttttatt ttcagaactg aacaggaaac 240
 238 gtcttcgcaa gtggatttct ctcagaccta agggttggaa tgatgttcgt ttggctgtga 300
 240 tcattgctgg atatcgcgag gatccttata tgttcagaa gtgcctcgag tctgtacgtg 360
 242 actctgatta tggcaacgtt gcccgctctga tttgtgtgat tgacggtgat gaggaacgat 420
 244 atatgaggat ggctgccgtt tacaaggcga tctacaatga taatatcaag aagcccagat 480
 246 ttgttctgtg tgagtcagac gacaagggaag gtgaacgcat cgactctgat ttctctcgcg 540
 248 acatttgtgt cctccagcct catcgtggaa aacgggagtg tctttatact gggtttcaac 600
 250 ttgcaaagat ggacccagat gtcaatgctg tcgttctgat tgacagcgat accgtttctg 660
 252 agaaggatgc tattctggaa gttgtatacc cacttgcatg cgatcccagag atccaagccg 720
 254 ttgcaggatga gtgtaagatt tggaacacag acactctttt gagtcttctc gtcgcttggc 780
 256 ggtactattc tgcgttttgt gtggagagga gtgccagtc ttttttcagg actgttcagt 840
 258 gcgttggggg gccactgggt gcctacaaga ttgatatcat taaggagatt aaggaccct 900

Invalid response - see error
 Summary sheet item 10

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Input Set : A:\sequence listing.txt

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| 260 | ggatttccca | gcgcttttctt | ggtcagaagt | gtacttacgg | tgacgaccgc | cggctaacca | 960 |
| 262 | acgagatctt | gatgcgtggt | aaaaagggtg | tgttcactcc | atttgctggt | ggttggtctg | 1020 |
| 264 | acagtccgac | caatgtgttt | cgttacatcg | ttcagcagac | ccgctggagt | aagtcgtggt | 1080 |
| 266 | gccgcgaaat | ttgttacacc | ctcttcgccg | cgtggaagca | cggtttgctc | ggaatttgcc | 1140 |
| 268 | tggcctttga | atgtttgtat | caaattacat | acttcttcct | cgtgatttac | ctcttttctc | 1200 |
| 270 | gcctagccgt | tgaggccgac | cctcgcgcc | agacagccac | ggtgattgtg | agcaccacgg | 1260 |
| 272 | ttgcattgat | taagtgtggg | tatttttcat | tccgagccaa | ggatattcgg | gcgttttact | 1320 |
| 274 | ttgtgcttta | tacatttggt | tactttttct | gtatgattcc | ggccaggatt | actgcaatga | 1380 |
| 276 | tgacgctttg | ggacattggc | tggggtactc | gcggtggaaa | cgagaagcct | tccgttgcca | 1440 |
| 278 | cccgggtcgc | tctgtgggca | aagcaatata | tcattgcata | tatgtggtgg | gccgcggttg | 1500 |
| 280 | ttggcgctgg | agtttacagc | atcgtccata | actggatggt | cgattggaat | tctctttctt | 1560 |
| 282 | atcgttttgc | tttggttggt | atttgttctt | acattgtttt | tattgttatt | gtgctggtgg | 1620 |
| 284 | tttatttcac | cggcaaaatt | acgacttggg | atttcacgaa | gcttcagaag | gagctaatac | 1680 |
| 286 | aggatcgctg | tctgtacgat | gcaactacca | atgctcagtc | tgtgtgattt | ttcctgcaag | 1740 |
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| 291 | <212> TYPE: DNA | | | | | | |
| 292 | <213> ORGANISM: Pastuerella Multocida | | | | | | |
| 294 | <400> SEQUENCE: 8 | | | | | | |
| 295 | attttttaag | gacagaaaat | gaatacatta | tcacaagcaa | taaaagcata | taacagcaat | 60 |
| 297 | gactatcaat | tagcactcaa | attatttgaa | aagtcggcgg | aaatctatgg | acggaaaatt | 120 |
| 299 | gttgaatttc | aaattaccaa | atgcaaaaga | aaactctcag | cacatccttc | tgtaatttca | 180 |
| 301 | gcacatcttt | ctgtaaaaaa | agaagaaaaa | gtcaatgttt | gcgatatgct | gttagatatt | 240 |
| 303 | gcaacacaac | tgttactttc | caacgtaaaa | aaattagtag | tttctgactc | ggaaaaaaac | 300 |
| 305 | acgttaaaaa | ataaatggaa | attgctcact | gagaagaaat | ctgaaaatgc | ggaggttaaga | 360 |
| 307 | gcggctcgcc | ttgtacccaa | agattttccc | aaagatctgg | ttttagcgcc | tttacctgat | 420 |
| 309 | catgttaatg | attttacatg | gtacaaaaag | cgaaagaaaa | gacttggcat | aaaacctgaa | 480 |
| 311 | catcaacatg | ttggctcttc | tattatcggt | acaacattca | atcgaccagc | aattttatcg | 540 |
| 313 | attacattag | cctgttttag | aaacccaaaa | acacattacc | cgtttgaagt | tatcgtgaca | 600 |
| 315 | gatgatggta | gtcaggaaga | tctatcaccg | atcattcgcc | aatatgaaaa | taaattggat | 660 |
| 317 | attcgctacg | tcagacaaaa | agataacggt | tttcaagcca | gtgccgctcg | gaatatggga | 720 |
| 319 | ttacgcttag | caaaatatga | ctttattggc | ttactcgact | gtgatatggc | gccaaatcca | 780 |
| 321 | ttatgggttc | attcttatgt | tgcagagcta | ttagaagatg | atgatttaac | aatcattggt | 840 |
| 323 | ccaagaaaat | acatcgatac | acaacatatt | gacccaaaag | acttcttaaa | taacgcgagt | 900 |
| 325 | ttgcttgaat | cattaccaga | agtgaaaacc | aataatagtg | ttgccgcaaa | aggggaagga | 960 |
| 327 | acagtttctc | tggattggcg | cttagaacia | ttcgaaaaaa | cagaaaatct | ccgcttatcc | 1020 |
| 329 | gattcgccct | tccgtttttt | tgcggcggtg | aatgttgctt | tcgctaaaaa | atggctaaat | 1080 |
| 331 | aaatccggtt | tctttgatga | ggaatttaat | cactgggggtg | gagaagatgt | ggaatttgga | 1140 |
| 333 | tatcgcttat | tccgttacgg | tagtttcttt | aaaactattg | atggcattat | ggcctaccat | 1200 |
| 335 | caagagccac | caggtaaaga | aatgaaacc | gatcgtgaag | cgggaaaaaa | tattacgctc | 1260 |
| 337 | gatattatga | gagaaaaggt | cccttatata | tatagaaaac | ttttaccaat | agaagattcg | 1320 |
| 339 | catatcaata | gagtaccttt | agtttcaatt | tatatccag | cttataactg | tgcaaaactat | 1380 |
| 341 | attcaacggt | gcgtagatag | tgcactgaat | cagactgttg | ttgatctcga | ggtttgattt | 1440 |
| 343 | tgtaacgatg | gttcaacaga | taatacctta | gaagtgatca | ataagcttta | tggttaataat | 1500 |
| 345 | cctaggggtac | gcatcatgtc | taaaccaaatt | ggcggaatag | cctcagcatc | aaatgcagcc | 1560 |
| 347 | gtttcttttg | ctaaagggtta | ttacattggg | cagtttagatt | cagatgatta | tcttgagcct | 1620 |
| 349 | gatgcagttg | aactgtgttt | aaaagaattt | ttaaaagata | aaacgctagc | ttgtgtttat | 1680 |
| 351 | accactaata | gaaacgtcaa | tccggatggg | agcttaatcg | ctaattggtta | caattggcca | 1740 |
| 353 | gaattttcac | gagaaaaaact | cacaacggct | atgattgctc | accactttag | aatgttcacg | 1800 |

RAW SEQUENCE LISTING

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Input Set : A:\sequenc listing.txt

Output Set: N:\CRF4\09052002\I469200C.raw

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357 gacatgttcc tcaaaactcag tgaagttgga aaattttaaac atcttaataa aatctgctat 1920
359 aaccgtgtat tacatggtga taacacatca attaagaaac ttggcattca aaagaaaaac 1980
361 cattttgttg tagtcaatca gtcattaaat agacaaggca taacttatta taattatgac 2040
363 gaatttgatg atttagatga aagtagaaag tatattttca ataaaaccgc tgaatatcaa 2100
365 gaagagattg atatcttaaa agatattaaa atcatccaga ataaagatgc caaaatcgca 2160
367 gtcagtattt tttatcccaa tacattaaac ggcttagtga aaaaactaaa caatattatt 2220
369 gaatataata aaaatatatt cgttattgtt ctacatgttg ataagaatca tcttacacca 2280
371 gatataaaaa aagaaataact agccttctat cataaacatc aagtgaatat tttactaaat 2340
373 aatgatatct catattacac gagtaataga ttaataaaaa ctgaggcgca ttttaagtaat 2400
375 attaataaat taagtcagtt aaatctaaat tgtgaataca tcatttttga taatcatgac 2460
377 agcctattcg ttaaaaaatga cagctatgct tatatgaaaa aatatgatgt cggcatgaat 2520
379 ttctcagcat taacacatga ttggatcgag aaaatcaatg cgcattccacc atttaaaaag 2580
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389 ctgacttata tgccttgagg aacgaaaatta caatggacaa atgaacaaat tgaaagtgca 2880
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394 <210> SEQ ID NO: 9

395 <211> LENGTH: 972

396 <212> TYPE: PRT

397 <213> ORGANISM: Pastuerella Multocida

399 <400> SEQUENCE: 9

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409 Lys Ile Val Glu Phe Gln Ile Thr Lys Cys Lys Glu Lys Leu Ser Ala
410 35 40 45
413 His Pro Ser Val Asn Ser Ala His Leu Ser Val Asn Lys Glu Glu Lys
414 50 55 60
417 Val Asn Val Cys Asp Ser Pro Leu Asp Ile Ala Thr Gln Leu Leu Leu
418 65 70 75 80
421 Ser Asn Val Lys Lys Leu Val Leu Ser Asp Ser Glu Lys Asn Thr Leu
422 85 90 95
425 Lys Asn Lys Trp Lys Leu Leu Thr Glu Lys Lys Ser Glu Asn Ala Glu
426 100 105 110
429 Val Arg Ala Val Ala Leu Val Pro Lys Asp Phe Pro Lys Asp Leu Val
430 115 120 125
433 Leu Ala Pro Leu Pro Asp His Val Asn Asp Phe Thr Trp Tyr Lys Lys
434 130 135 140
437 Arg Lys Lys Arg Leu Gly Ile Lys Pro Glu His Gln His Val Gly Leu
438 145 150 155 160
441 Ser Ile Ile Val Thr Thr Phe Asn Arg Pro Ala Ile Leu Ser Ile Thr
442 165 170 175
445 Leu Ala Cys Leu Val Asn Gln Lys Thr His Tyr Pro Phe Glu Val Ile
446 180 185 190
449 Val Thr Asp Asp Gly Ser Gln Glu Asp Leu Ser Pro Ile Ile Arg Gln

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VERIFICATION SUMMARY

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